

Re-reqs

RAW SEQUENCE LISTING

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Application Serial Number: 10/019,368
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PATENT APPLICATION: US/10/019,368

DATE: 08/05/2005

TIME: 10:59:47

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\08042005\J019368.raw

4 <110> APPLICANT: Dean, Nicholas M.
 5 ISIS PHARMACEUTICALS, INC.
 7 <120> TITLE OF INVENTION: Antisense Oligonucleotide Modulation of Human Protein
 8 Kinase C-delta Expression
 10 <130> FILE REFERENCE: ISPH-0458
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/019,368
 C--> 12 <141> CURRENT FILING DATE: 2001-11-13
 12 <150> PRIOR APPLICATION NUMBER: US 09/313,930
 13 <151> PRIOR FILING DATE: 1999-05-18
 16 <160> NUMBER OF SEQ ID NOS: 20
 18 <170> SOFTWARE: PatentIn Ver. 2.0
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 2104
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Homo sapiens
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (59)..(2089)
 29 <300> PUBLICATION INFORMATION:
 30 <301> AUTHORS: Aris, J . P.
 31 Basta, P. V.
 32 Holmes, W. D.
 33 Ballas, L. M.
 34 Moomaw, C.
 35 Rankl, N. B.
 36 Blöbel, G.
 37 Loomis, C. R.
 38 Burns, D. J.
 39 <302> TITLE: Molecular and biochemical characterization of a
 40 recombinant human PKC-delta family member
 41 <303> JOURNAL: Biochim. Biophys. Acta
 42 <304> VOLUME: 1174
 43 <305> ISSUE: 2
 44 <306> PAGES: 171-181
 45 <307> DATE: 1993-08-19
 46 <308> DATABASE ACCESSION NO: L07860
 47 <309> DATABASE ENTRY DATE: 1993-11-02
 49 <400> SEQUENCE: 1
 50 tgccggcgcc acccttggcg cctgccccctg caacgggagc cccactgcag gccccacc 58
 52 atg gcg ccg ttc ctg cgc atc gcc ttc aac tcc tat gag ctg ggc tcc 106
 53 Met Ala Pro Phe Leu Arg Ile Ala Phe Asn Ser Tyr Glu Leu Gly Ser
 54 1 5 10 15
 56 ctg cag gcc gag gac gag gcg aac cag ccc ttc tgt gcc gtg aag atg 154

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57	Leu Gln Ala Glu Asp Glu Ala Asn Gln Pro Phe Cys Ala Val Lys Met			
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60	aag gag gcg ctc agc aca gag cgt ggg aaa aca ctg gtg cag aag aag	202		
61	Lys Glu Ala Leu Ser Thr Glu Arg Gly Lys Thr Leu Val Gln Lys Lys			
62	35	40	45	
64	ccg acc atg tat cct gag tgg aag tcg acg ttc gat gcc cac atc tat	250		
65	Pro Thr Met Tyr Pro Glu Trp Lys Ser Thr Phe Asp Ala His Ile Tyr			
66	50	55	60	
68	gag ggg cgc gtc atc cag att gtg cta atg cgg gca gca gag gag cca	298		
69	Glu Gly Arg Val Ile Gln Ile Val Leu Met Arg Ala Ala Glu Glu Pro			
70	70	75	80	
72	gtg tct gag gtg acc gtg ggt gtg tcg gtg gcc gag cgc tgc aag	346		
73	Val Ser Glu Val Thr Val Gly Val Ser Val Leu Ala Glu Arg Cys Lys			
74	85	90	95	
76	aag aac aat ggc aag gct gag ttc tgg ctg gac ctg cag cct cag gcc	394		
77	Lys Asn Asn Gly Lys Ala Glu Phe Trp Leu Asp Leu Gln Pro Gln Ala			
78	100	105	110	
80	aag gtg ttg atg tct gtt cag tat ttc ctg gag gac gtg gat tgc aaa	442		
81	Lys Val Leu Met Ser Val Gln Tyr Phe Leu Glu Asp Val Asp Cys Lys			
82	115	120	125	
84	caa tct atg cgc agt gag gac gag gac aag ttc cca acg atg aac cgc	490		
85	Gln Ser Met Arg Ser Glu Asp Glu Ala Lys Phe Pro Thr Met Asn Arg			
86	130	135	140	
88	cgc gga gcc atc aaa cag gcc aaa atc cac tac atc aag aac cat gag	538		
89	Arg Gly Ala Ile Lys Gln Ala Lys Ile His Tyr Ile Lys Asn His Glu			
90	145	150	155	160
92	ttt atc gcc acc ttc ttt ggg caa ccc acc ttc tgt tct gtg tgc aaa	586		
93	Phe Ile Ala Thr Phe Phe Gly Gln Pro Thr Phe Cys Ser Val Cys Lys			
94	165	170	175	
96	gac ttt gtc tgg ggc ctc aac aag caa ggc tac aaa tgc agg caa tgt	634		
97	Asp Phe Val Trp Gly Leu Asn Lys Gln Gly Tyr Lys Cys Arg Gln Cys			
98	180	185	190	
100	aac gct gcc atc cac aag aaa tgc atc gac aag atc atc ggc aga tgc	682		
101	Asn Ala Ala Ile His Lys Lys Cys Ile Asp Lys Ile Ile Gly Arg Cys			
102	195	200	205	
104	act ggc acc gcg gcc aac agc cgg gac act ata ttc cag aaa gaa cgc	730		
105	Thr Gly Thr Ala Ala Asn Ser Arg Asp Thr Ile Phe Gln Lys Glu Arg			
106	210	215	220	
108	ttc aac atc gac atg cgg cac cgc ttc aag gtt cac aac tac atg agc	778		
109	Phe Asn Ile Asp Met Pro His Arg Phe Lys Val His Asn Tyr Met Ser			
110	225	230	235	240
112	ccc acc ttc tgt gac cac tgc ggc agc ctg ctc tgg gga ctg gtg aag	826		
113	Pro Thr Phe Cys Asp His Cys Gly Ser Leu Leu Trp Gly Leu Val Lys			
114	245	250	255	
116	cag gga tta aag tgt gaa gac tgc ggc atg aat gtg cac cat aaa tgc	874		
117	Gln Gly Leu Lys Cys Glu Asp Cys Gly Met Asn Val His His Lys Cys			
118	260	265	270	
120	cgg gag aag gtg gcc aac ctc tgc ggc atc aac cag aag ctt ttg gct	922		
121	Arg Glu Lys Val Ala Asn Leu Cys Gly Ile Asn Gln Lys Leu Ala			

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128	gcc tcc tca gag cct gtt ggg ata tat cag ggt ttc gag aag aag acc			1018
129	Ala Ser Ser Glu Pro Val Gly Ile Tyr Gln Gly Phe Glu Lys Lys Thr			
130	305	310	315	320
132	gga gtt gct ggg gag gac atg caa gac aac agt ggg acc tac ggc aag			1066
133	Gly Val Ala Gly Asp Met Gln Asp Asn Ser Gly Thr Tyr Gly Lys			
134	325	330	335	
136	atc tgg gag ggc agc agc aag tgc aac atc aac ttc atc ttc cac			1114
137	Ile Trp Glu Gly Ser Ser Lys Cys Asn Ile Asn Asn Phe Ile Phe His			
138	340	345	350	
140	aag gtc ctg ggc aaa ggc agc ttc ggg aag gtg ctg ctt gga gag ctg			1162
141	Lys Val Leu Gly Lys Gly Ser Phe Gly Lys Val Leu Leu Gly Glu Leu			
142	355	360	365	
144	aag ggc aga gga gag tac tct gcc atc aag gcc ctc aag aag gat gtg			1210
145	Lys Gly Arg Gly Glu Tyr Ser Ala Ile Lys Ala Leu Lys Lys Asp Val			
146	370	375	380	
148	gtc ctg atc gac gac gtg gag tgc acc atg gtt gag aag cgg gtg			1258
149	Val Leu Ile Asp Asp Val Glu Cys Thr Met Val Glu Lys Arg Val			
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152	ctg aca ctt gcc gca gag aat ccc ttt ctc acc cac ctc atc tgc acc			1306
153	Leu Thr Leu Ala Ala Glu Asn Pro Phe Leu Thr His Leu Ile Cys Thr			
154	405	410	415	
156	ttc cag acc aag gac cac ctg ttc ttt gtg atg gag ttc ctc aac ggg			1354
157	Phe Gln Thr Lys Asp His Leu Phe Phe Val Met Glu Phe Leu Asn Gly			
158	420	425	430	
160	ggg gac ctg atg tac cac atc cag gac aaa ggc cgc ttt gaa ctc tac			1402
161	Gly Asp Leu Met Tyr His Ile Gln Asp Lys Gly Arg Phe Glu Leu Tyr			
162	435	440	445	
164	cgt gcc acg ttt tat gcc gct gag ata atg tgt gga ctg cag ttt cta			1450
165	Arg Ala Thr Phe Tyr Ala Ala Glu Ile Met Cys Gly Leu Gln Phe Leu			
166	450	455	460	
168	cac agc aag ggc atc att tac agg gac ctc aaa ctg gac aat gtg ctg			1498
169	His Ser Lys Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn Val Leu			
170	465	470	475	480
172	ttg gac cgg gat ggc cac atc aag att gcc gac ttt ggg atg tgc aaa			1546
173	Leu Asp Arg Asp Gly His Ile Lys Ile Ala Asp Phe Gly Met Cys Lys			
174	485	490	495	
176	gag aac ata ttc ggg gag agc cgg gcc agc acc ttc tgc ggc acc cct			1594
177	Glu Asn Ile Phe Gly Glu Ser Arg Ala Ser Thr Phe Cys Gly Thr Pro			
178	500	505	510	
180	gac tat atc gcc cct gag atc cta cag ggc ctg aag tac aca ttc tct			1642
181	Asp Tyr Ile Ala Pro Glu Ile Leu Gln Gly Leu Lys Tyr Thr Phe Ser			
182	515	520	525	
184	gtg gac tgg tgg tct ttc ggg gtc ctt ctg tac gag atg ctc att ggc			1690
185	Val Asp Trp Trp Ser Phe Gly Val Leu Leu Tyr Glu Met Leu Ile Gly			
186	530	535	540	

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188	cag tcc ccc ttc cat ggt gat gat gag gag tcc ttc gag tcc atc	1738
189	Gln Ser Pro Phe His Gly Asp Asp Glu Asp Glu Leu Phe Glu Ser Ile	
190	545 550 555 560	
192	cgt gtg gac acg cca cat tat ccc cgc tgg atc acc aag gag tcc aag	1786
193	Arg Val Asp Thr Pro His Tyr Pro Arg Trp Ile Thr Lys Glu Ser Lys	
194	565 570 575	
196	gac atc ctg gag aag ctc ttt gaa agg gaa cca acc aag agg ctg gga	1834
197	Asp Ile Leu Glu Lys Leu Phe Glu Arg Glu Pro Thr Lys Arg Leu Gly	
198	580 585 590	
200	atg acg gga aac atc aaa atc cac ccc ttc ttc aag acc ata aac tgg	1882
201	Met Thr Gly Asn Ile Lys Ile His Pro Phe Phe Lys Thr Ile Asn Trp	
202	595 600 605	
204	act ctg ctg gaa aag cgg agg ttg gag cca ccc ttc agg ccc aaa gtg	1930
205	Thr Leu Leu Glu Lys Arg Arg Leu Glu Pro Pro Phe Arg Pro Lys Val	
206	610 615 620	
208	aag tca ccc aga gac tac agt aac ttt gac cag gag ttc ctg aac gag	1978
209	Lys Ser Pro Arg Asp Tyr Ser Asn Phe Asp Gln Glu Phe Leu Asn Glu	
210	625 630 635 640	
212	aag gcg cgc ctc tcc tac agc gac aag aac ctc atc gac tcc atg gac	2026
213	Lys Ala Arg Leu Ser Tyr Ser Asp Lys Asn Leu Ile Asp Ser Met Asp	
214	645 650 655	
216	cag tct gca ttc gtc ggc ttc tcc ttt gtg aac aac ccc aaa ttc gag cac	2074
217	Gln Ser Ala Phe Ala Gly Phe Ser Phe Val Asn Pro Lys Phe Glu His	
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235	20 25 30	
237	Lys Glu Ala Leu Ser Thr Glu Arg Gly Lys Thr Leu Val Gln Lys Lys	
238	35 40 45	
240	Pro Thr Met Tyr Pro Glu Trp Lys Ser Thr Phe Asp Ala His Ile Tyr	
241	50 55 60	
243	Glu Gly Arg Val Ile Gln Ile Val Leu Met Arg Ala Ala Glu Glu Pro	
244	65 70 75 80	
246	Val Ser Glu Val Thr Val Gly Val Ser Val Leu Ala Glu Arg Cys Lys	
247	85 90 95	
249	Lys Asn Asn Gly Lys Ala Glu Phe Trp Leu Asp Leu Gln Pro Gln Ala	
250	100 105 110	
252	Lys Val Leu Met Ser Val Gln Tyr Phe Leu Glu Asp Val Asp Cys Lys	
253	115 120 125	
255	Gln Ser Met Arg Ser Glu Asp Glu Ala Lys Phe Pro Thr Met Asn Arg	

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256	130	135	140
258	Arg Gly Ala Ile Lys Gln Ala Lys Ile His Tyr Ile Lys Asn His Glu		
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261	Phe Ile Ala Thr Phe Phe Gly Gln Pro Thr Phe Cys Ser Val Cys Lys		160
262	165	170	175
264	Asp Phe Val Trp Gly Leu Asn Lys Gln Gly Tyr Lys Cys Arg Gln Cys		
265	180	185	190
267	Asn Ala Ala Ile His Lys Lys Cys Ile Asp Lys Ile Ile Gly Arg Cys		
268	195	200	205
270	Thr Gly Thr Ala Ala Asn Ser Arg Asp Thr Ile Phe Gln Lys Glu Arg		
271	210	215	220
273	Phe Asn Ile Asp Met Pro His Arg Phe Lys Val His Asn Tyr Met Ser		
274	225	230	235
276	Pro Thr Phe Cys Asp His Cys Gly Ser Leu Leu Trp Gly Leu Val Lys		240
277	245	250	255
279	Gln Gly Leu Lys Cys Glu Asp Cys Gly Met Asn Val His His Lys Cys		
280	260	265	270
282	Arg Glu Lys Val Ala Asn Leu Cys Gly Ile Asn Gln Lys Leu Leu Ala		
283	275	280	285
285	Glu Ala Leu Asn Gln Val Thr Gln Arg Ala Ser Arg Arg Ser Asp Ser		
286	290	295	300
288	Ala Ser Ser Glu Pro Val Gly Ile Tyr Gln Gly Phe Glu Lys Lys Thr		
289	305	310	315
291	Gly Val Ala Gly Glu Asp Met Gln Asp Asn Ser Gly Thr Tyr Gly Lys		320
292	325	330	335
294	Ile Trp Glu Gly Ser Ser Lys Cys Asn Ile Asn Asn Phe Ile Phe His		
295	340	345	350
297	Lys Val Leu Gly Lys Gly Ser Phe Gly Lys Val Leu Leu Gly Glu Leu		
298	355	360	365
300	Lys Gly Arg Gly Glu Tyr Ser Ala Ile Lys Ala Leu Lys Lys Asp Val		
301	370	375	380
303	Val Leu Ile Asp Asp Asp Val Glu Cys Thr Met Val Glu Lys Arg Val		
304	385	390	395
306	Leu Thr Leu Ala Ala Glu Asn Pro Phe Leu Thr His Leu Ile Cys Thr		400
307	405	410	415
309	Phe Gln Thr Lys Asp His Leu Phe Phe Val Met Glu Phe Leu Asn Gly		
310	420	425	430
312	Gly Asp Leu Met Tyr His Ile Gln Asp Lys Gly Arg Phe Glu Leu Tyr		
313	435	440	445
315	Arg Ala Thr Phe Tyr Ala Ala Glu Ile Met Cys Gly Leu Gln Phe Leu		
316	450	455	460
318	His Ser Lys Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn Val Leu		
319	465	470	475
321	Leu Asp Arg Asp Gly His Ile Lys Ile Ala Asp Phe Gly Met Cys Lys		480
322	485	490	495
324	Glu Asn Ile Phe Gly Glu Ser Arg Ala Ser Thr Phe Cys Gly Thr Pro		
325	500	505	510
327	Asp Tyr Ile Ala Pro Glu Ile Leu Gln Gly Leu Lys Tyr Thr Phe Ser		
328	515	520	525

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PTO/STIC

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/019,368

DATE: 08/05/2005

TIME: 10:59:48

Input Set : A:\PTO.AMC.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date